

## APPENDIX E



## lalign output for 2 vs. 3

[ISREC-Server] Date: Thu May 23 4:50:04 MET 2002

./wwwtmp/lalign/.1489.1.seq : 3841 aa

ALIGN calculates a global alignment of two sequences  
version 2.0uPlease cite: Myers and Miller, CABIOS (1989) 4:11-17

2 3841 aa vs.  
3 3841 aa

scoring matrix: BLOSUM50, gap penalties: -14/-4  
100.0% identity; Global alignment score: 24253

|        | 10  | 20  | 30 | 40 | 50 | 60 |
|--------|---|---|----|----|----|----|
| ./wwwt | METALAHISSELYSTHRARGTHRASNAPGLYLYSILETHRTYRPRPRGLYVALLYSGL      | ::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: |    |    |    |    |
| 3      | METALAHISSELYSTHRARGTHRASNAPGLYLYSILETHRTYRPRPRGLYVALLYSGL      | 10 20 30 40 50 60   |    |    |    |    |
|        | 70 80 90 100 110 120  |   |    |    |    |    |
| ./wwwt | ILESERASPLYSILESERLYSGLGLMETVALARGARGLELYSMETVALVALLYSTHRPHE    | ::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: |    |    |    |    |
| 3      | ILESERASPLYSILESERLYSGLGLMETVALARGARGLELYSMETVALVALLYSTHRPHE    | 70 80 90 100 110 120  |    |    |    |    |
|        | 130 140 150 160 170 180   |   |    |    |    |    |
| ./wwwt | METASPMETASPGLNASP SERGLGLLYSGLLETYRLEASNLEALALEHISLEALASER     | ::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: |    |    |    |    |
| 3      | METASPMETASPGLNASP SERGLGLLYSGLLETYRLEASNLEALALEHISLEALASER     | 130 140 150 160 170 180   |    |    |    |    |
|        | 190 200 210 220 230 240   |   |    |    |    |    |
| ./wwwt | ASPPHEPHELELYSHISPRGLYLYSASPVALARGLELEVALALACYSCSLEALAASPIL     | ::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: |    |    |    |    |
| 3      | ASPPHEPHELELYSHISPRGLYLYSASPVALARGLELEVALALACYSCSLEALAASPIL     | 190 200 210 220 230 240   |    |    |    |    |
|        | 250 260 270 280 290 300   |   |    |    |    |    |
| ./wwwt | EPHEARGILETYRALAPRGLALAPRTYRTHR SERPRASPLYSLELYSASP ILEPHEMETP  | ::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: |    |    |    |    |
| 3      | EPHEARGILETYRALAPRGLALAPRTYRTHR SERPRASPLYSLELYSASP ILEPHEMETP  | 250 260 270 280 290 300   |    |    |    |    |
|        | 310 320 330 340 350 360   |   |    |    |    |    |
| ./wwwt | HEILETHRARGGLNLELYSGLYLEGGLASPTHRLYSSERPRGLNPHEASNARGTYRPHETY   | ::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: |    |    |    |    |
| 3      | HEILETHRARGGLNLELYSGLYLEGGLASPTHRLYSSERPRGLNPHEASNARGTYRPHETY   | 310 320 330 340 350 360   |    |    |    |    |
|        | 370 380 390 400 410 420   |   |    |    |    |    |
| ./wwwt | RLELEGGLASNILEALATRPVALLYSSERTYRASNILECYSPHEGLLEGGLASP SERASNGL | ::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: |    |    |    |    |
| 3      | RLELEGGLASNILEALATRPVALLYSSERTYRASNILECYSPHEGLLEGGLASP SERASNGL | 370 380 390 400 410 420   |    |    |    |    |
|        | 430 440 450 460 470 480   |   |    |    |    |    |
| ./wwwt | ILEPHEHTRGLNLETYRARGTHRLEPHESERVALILEASN ASNGLYHISASNGLNLYSVA   | ::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: ::::::::::::::::::::: |    |    |    |    |

3 ILEPHETHRGLNLETYRARGTHRLEPHESERVALILEASNASNGLYHISASNGLNLYSVA  
430 440 450 460 470 480  
490 500 510 520 530 540  
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550 560 570 580 590 600  
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610 620 630 640 650 660  
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610 620 630 640 650 660  
670 680 690 700 710 720  
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670 680 690 700 710 720  
730 740 750 760 770 780  
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730 740 750 760 770 780  
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3 RASNASPASNGLGLARGLEGlnVALVALLYSLEALALYSMETPHEGLYALALYSASPS  
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910 920 930 940 950 960  
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970 980 990 1000 1010 1020  
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3 LYSASPLETHRGRLTYRLELYSVALARGSERHISASPPRGLGLALAILEARGHISASPV  
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1810 1820 1830 1840 1850 1860
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1810 1820 1830 1840 1850 1860

1870 1880 1890 1900 1910 1920
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1870 1880 1890 1900 1910 1920

1930 1940 1950 1960 1970 1980
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1990 2000 2010 2020 2030 2040
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2050 2060 2070 2080 2090 2100
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2110 2120 2130 2140 2150 2160
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2170 2180 2190 2200 2210 2220
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2230 2240 2250 2260 2270 2280
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2290 2300 2310 2320 2330 2340
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2350 2360 2370 2380 2390 2400
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2350 2360 2370 2380 2390 2400

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2410 2420 2430 2440 2450 2460  
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3 YLYSILESERLYSPRASPMETSERARGLEARGLAALAGLYSERALAILEVALLYSLE  
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2470 2480 2490 2500 2510 2520  
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3 ALAGLNLPRCYSTYRHISGLILEILETHRLEGLGLNTYRGLNLECYSSALALEALAILEA  
2470 2480 2490 2500 2510 2520  
  
2530 2540 2550 2560 2570 2580  
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2590 2600 2610 2620 2630 2640  
  
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2950 2960 2970 2980 2990 3000  
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2950 2960 2970 2980 2990 3000  
  
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3070 3080 3090 3100 3110 3120  
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3190 3200 3210 3220 3230 3240  
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3190 3200 3210 3220 3230 3240  
3250 3260 3270 3280 3290 3300  
. /wwwt LYSGLYARGLEASP SERG LMETASP HISSE RGLAS NGLAS PTYRTHRMETSER SERP  
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3250 3260 3270 3280 3290 3300  
3310 3320 3330 3340 3350 3360  
. /wwwt RLEPRGLYLYS LYSSER ASPL YSARGASP ASPSERAS PLEVAL ARGSE RLLEG LLYSPR  
3 RLEPRGLYLYS LYSSER ASPL YSARGASP ASPSERAS PLEVAL ARGSE RLLEG LLYSPR  
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3370 3380 3390 3400 3410 3420  
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3 ARGG LYARGL YSLY STHR PRV ALTH RGL GLNL LYSLEG LYMETASPAS PLETH RLYS  
3370 3380 3390 3400 3410 3420  
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. /wwwt GLGLP RT H RMETLYSTHR SERLYS L YSGLYSERLYSL YSSER GLYPR P RALAP RGL G  
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. /wwwt LGLGLGLGLARGGLN SERGLYASNTH RGL GLNLYSSERLYS GLN HISARGVA  
3 LGLGLGLGLARGGLN SERGLYASNTH RGL GLNLYSSERLYS GLN HISARGVA

|        |      |                      |                    |                     |                     |          |
|--------|------|----------------------|--------------------|---------------------|---------------------|----------|
|        | 3670 | 3680                 | 3690               | 3700                | 3710                | 3720     |
|        | 3730 | 3740                 | 3750               | 3760                | 3770                | 3780     |
| ./wwwt | L    | SERARGAGLNLNARGALAGL | SERPRGLSER         | SERALAILEGL         | SERTHRGLNSER        |          |
|        | 3730 | 3740                 | 3750               | 3760                | 3770                | 3780     |
| 3      | L    | SERARGAGLNLNARGALAGL | SERPRGLSER         | SERALAILEGL         | SERTHRGLNSER        |          |
|        | 3730 | 3740                 | 3750               | 3760                | 3770                | 3780     |
|        | 3790 | 3800                 | 3810               | 3820                | 3830                | 3840     |
| ./wwwt | T    | HPRGLNLYSGLYARGGLY   | ARGPRSERLYSTH      | RPRSERPRSERGLNPRLYS | LYSASNVA            |          |
|        | 3790 | 3800                 | 3810               | 3820                | 3830                | 3840     |
| 3      | L    | T                    | HPRGLNLYSGLYARGGLY | ARGPRSERLYSTH       | RPRSERPRSERGLNPRLYS | LYSASNVA |
|        | 3790 | 3800                 | 3810               | 3820                | 3830                | 3840     |

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